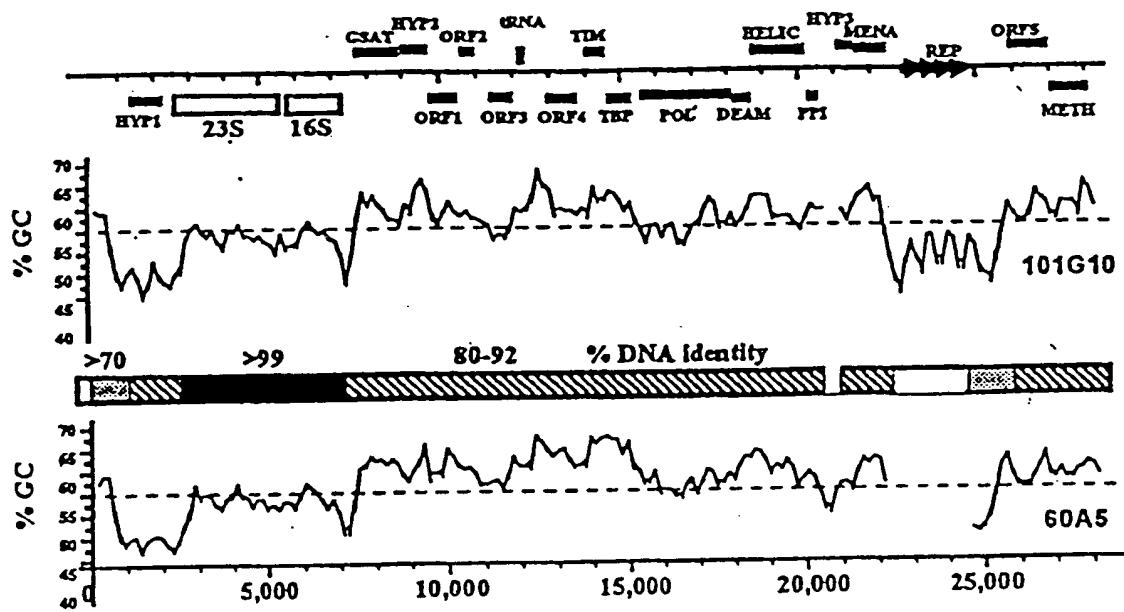


FIGURE 1



10027306 - 122401

Figure 2

Eq. No.	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)	
81	Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGCGCATG	-----	-----	25
82		B	AAGCTAAACT TTTAAT TGGG ATCCGGCGAG CCGGCGCGTG	-----	-----	
83	Hypoth 02	A	GGAAACTTTG ATTATA CGGG CGTGCTGCC CGGGGCCAT G-----	-----	-----	26
84		B	GGAAACTTTG ATTATA CGGG CGTACATTCC CGGGGCCAT G-----	-----	-----	
85	ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCCGTCTGT AACGGCCGTA TG-----	-----	-----	27
86		B	ACGGCAAGGT AATAAT AGCC TGCCGTCCGT ACCTGCCGTA TG-----	-----	-----	
87	ORF 03	A	CATGGAACTA GATATT AACC GGTTCGCAGG ATCCCAGTCA TG-----	-----	-----	27
88		B	CATGGAACTA GATAAT AACC GGTCCGCAGG GTACAATGCA TG-----	-----	-----	
89	PPI	A	ATACCGAGAA GTTATA GCAG GGTATGGAAT GTGCGCGC ATG-----	-----	-----	28
90		B	AGCACGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG-----	-----	-----	
91	GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG GCCTGCTGCC GTG-----	-----	-----	28
92		B	ATCCGGCCTC ATTAAA TTAC GGGGGGTACA ACCTGCTGCC GTG-----	-----	-----	
93	ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT GCGGCTGCC ATG-----	-----	-----	28
94		B	ACTTCATACA CATAAA TCCC GCCTGAACGG TCGTCCGCC ATG-----	-----	-----	
95	deaminase	A	.GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGCC GTG-----	-----	-----	29
96		B	CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCC .GTG-----	-----	-----	
97	RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT CAGGCCGCG CGTG-----	-----	-----	29
98		B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG CAGGCCG .CG CGTG-----	-----	-----	
99	ORF 06	A	..ACACGCAG TATAAA CGGG GGGCGGGCG GCGCGTATCA CATG-----	-----	-----	29
100		B	ATACACGTGG TATAAA CAGA GG .CCGGACG GCGCGGACCA CATG-----	-----	-----	
101	tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT CACGGATCGT CCCA-----	-----	-----	29
102		B	GCGATAGTTA TTTAAA ACTA GGATGCCGG CACCGTCGT CCCA-----	-----	-----	
103	TBP	A	CCGGGCCCG GTTAAA ATAG CG .CACGGGC GGATCCTGAC CAATG-----	-----	-----	30
104		B	CCGGGCCCG GTTAAA ATAG AGTGCGGCCG GGCACCGGAT CAATG-----	-----	-----	
105	TIM	A	GCGTCGATAG AATAAA TACG CGCAGGGGC CCCGTGGCGC GATGCCCGT G-----	-----	-----	36
106		B	GCGTCGATAG AATAAA TACG CGC .GGGGCC GCGGTGC . GATGCCCGT G-----	-----	-----	
107	Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG	-----	45	
108		B	ACTTCAACTA CATAAA TGCC TAGCTACGCA GAAATATCAA ACAAAAGTACT TCGACTAATG	-----		
109	ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCCCTTGCGT TGTA // .G CGGGGTGCC CAGGGGATG	-----	52	
110		B	ACGGCAGGCT ATTATT ACCT TGCCGTGTG . TACA // .G AGGGGGCCTG CCGGGAGTG	-----		
111	Methylase	A	CTACAACGAT TTTAAG TCGG CGCCGGGGCA GCCG .// .G ATGTGGGCCA GGCAACATG	-----	104	
112		B	CTACAAAGAT TTTAAG ACGG CGCGGGTGCC GCGG .// .T GGCACGGGG CCTATCTTG	-----		
113	16S RNA	A	TCGGCGATGG TTTATA TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC .// .AAT	-----	220	
114		B	CCGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC .// .AAT	-----		
	Archaeal promoter consensus		YTTAWA			

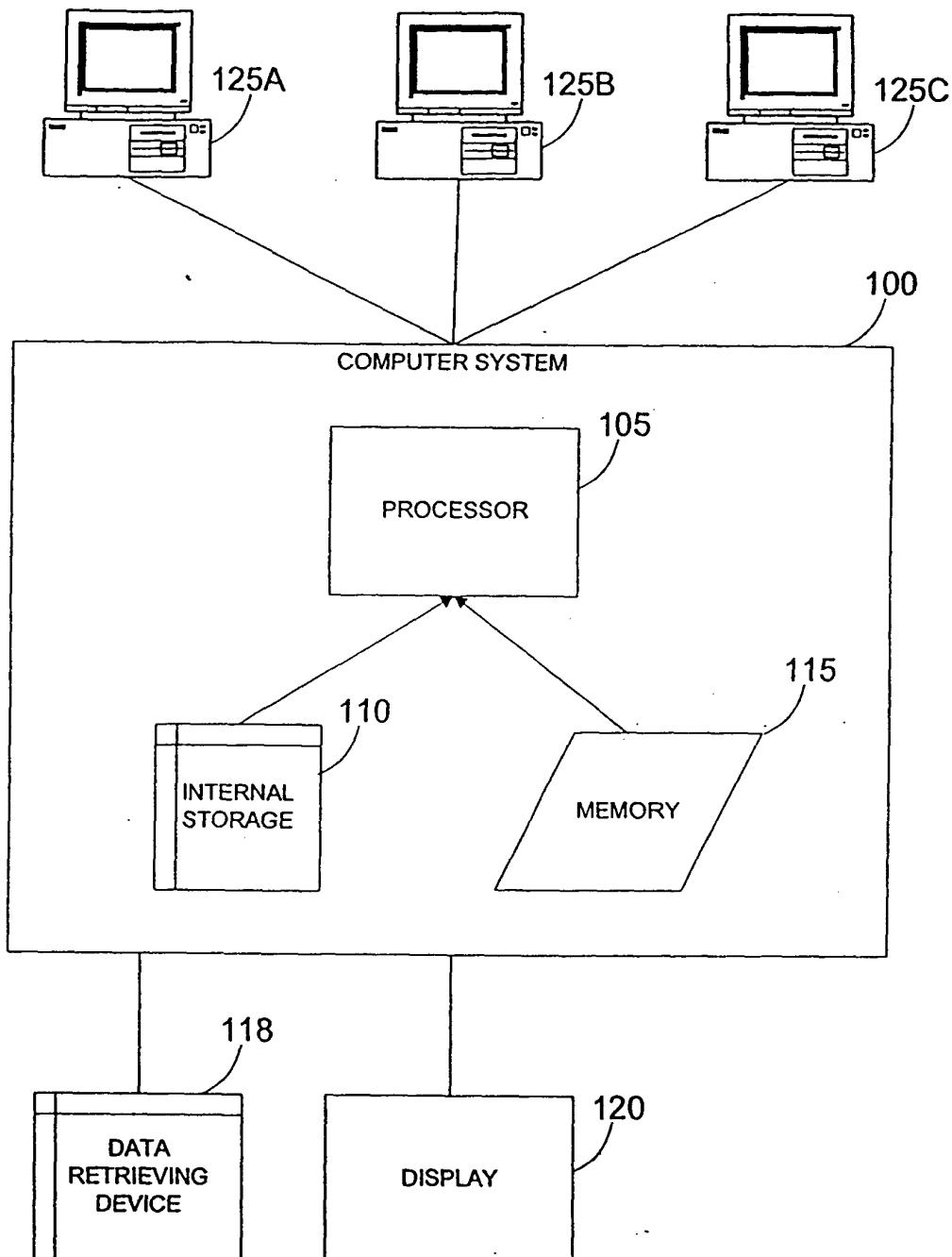
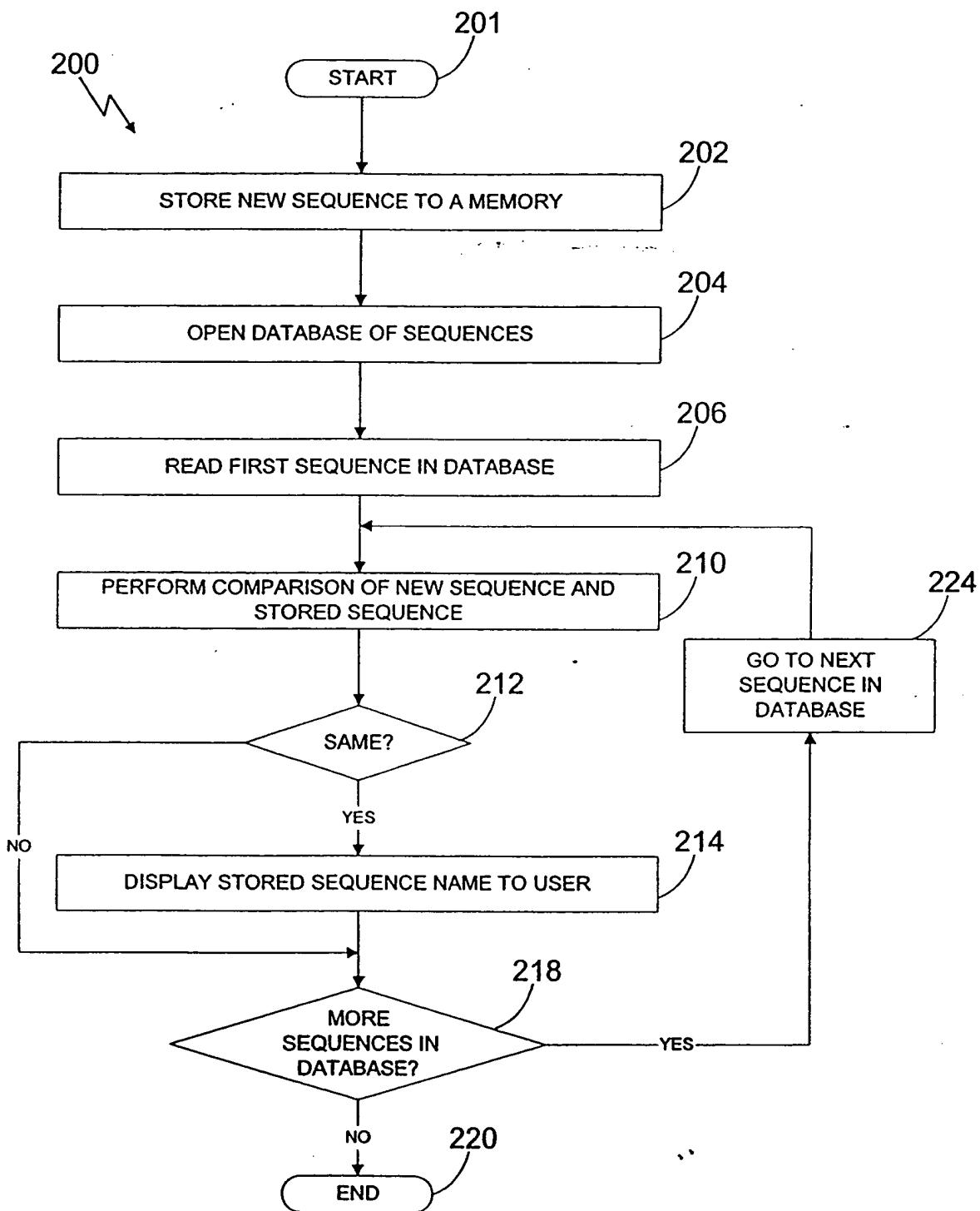


FIGURE 3

**FIGURE 4**

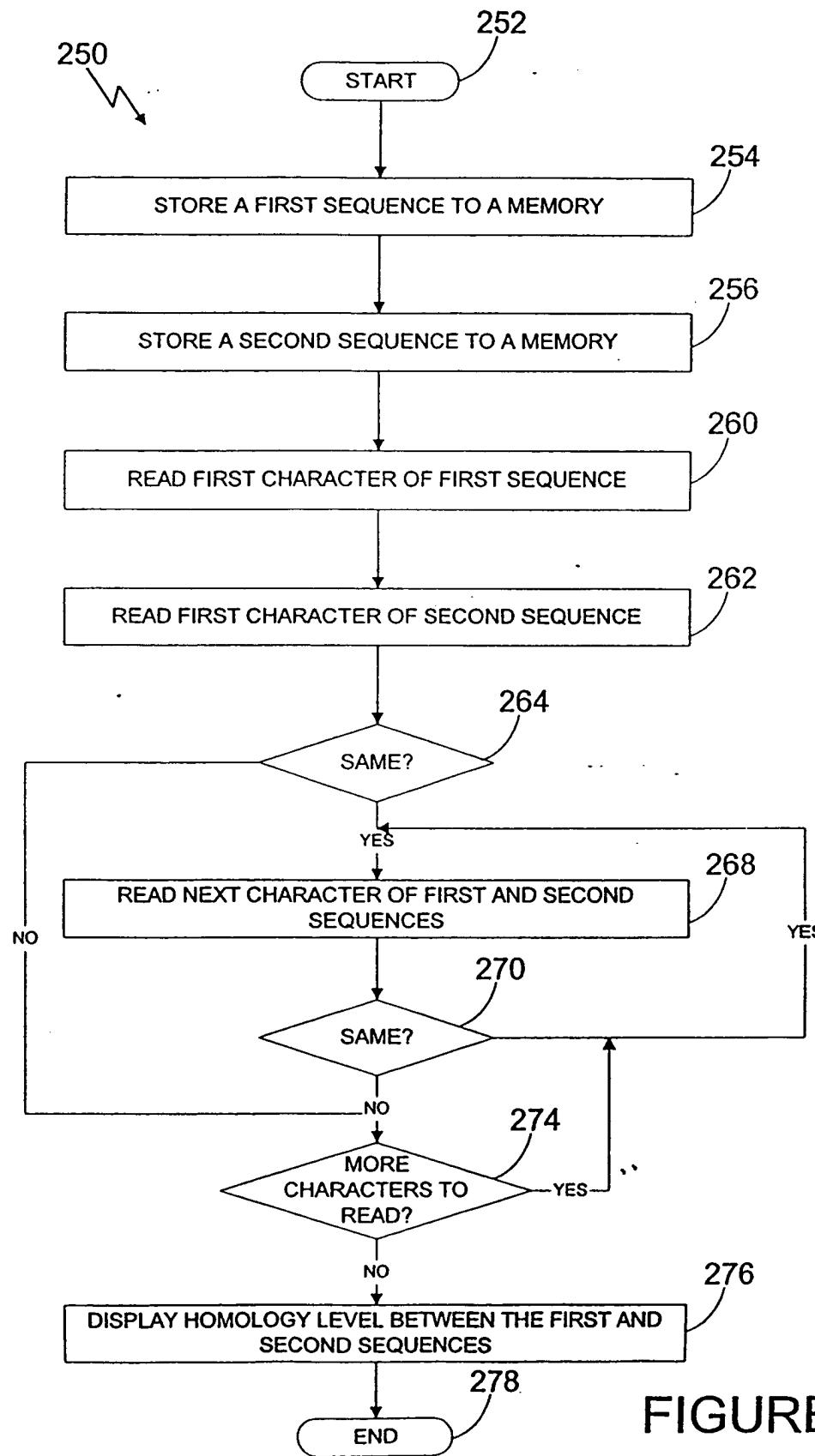


FIGURE 5

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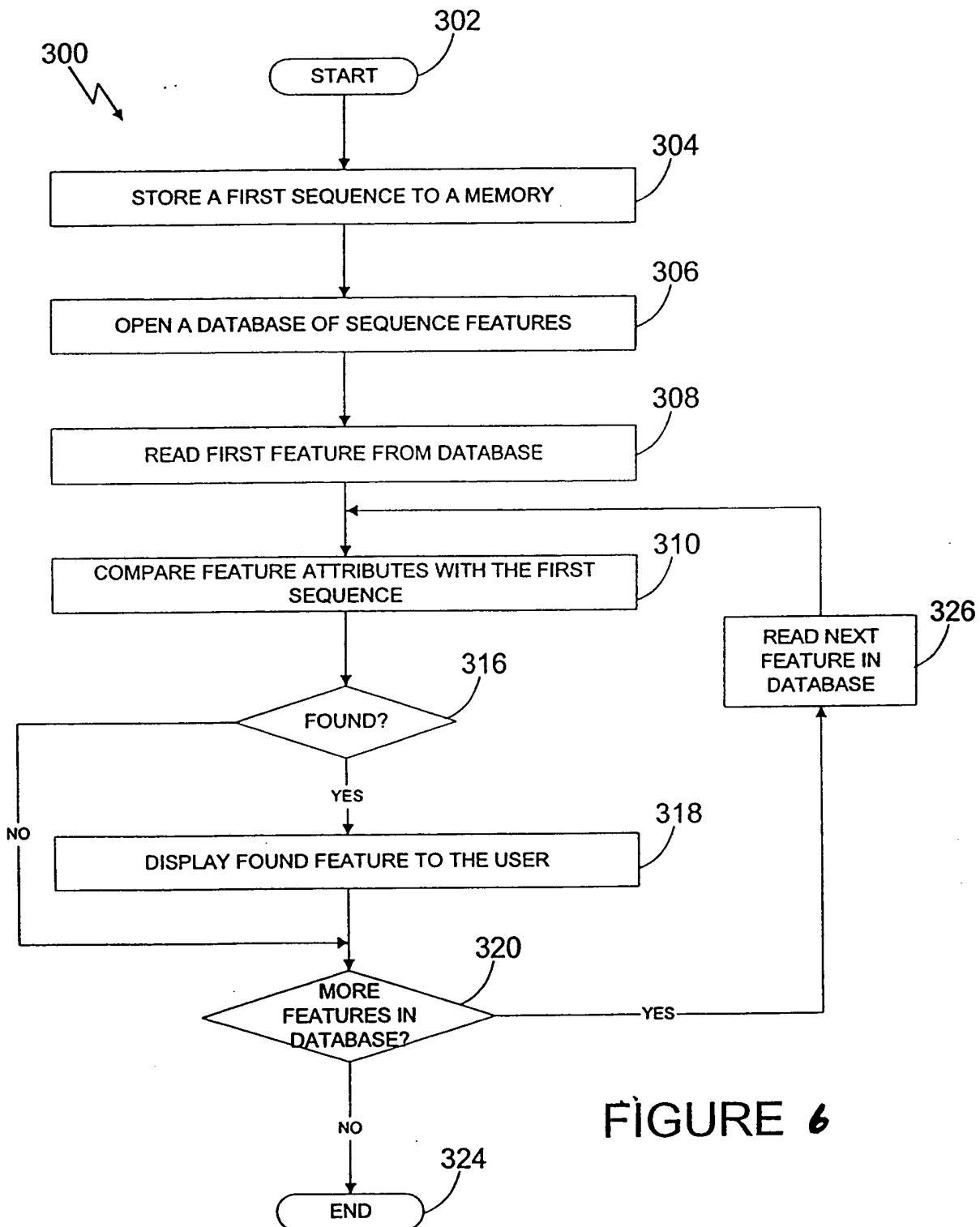


FIGURE 6